What is claimed is:

1. A composition capable of inhibiting specific binding between a signal-transducing protein and a cytoplasmic protein containing the amino acid sequence (G/S/A/E)-L-G-(F/I/L), wherein each - represents a peptide bond, each parenthesis encloses amino acids which are alternatives to one other, and each slash within such parentheses separating the alternative amino acids.

2. The composition of claim 1, wherein the cytoplasmic protein contains the amino acid sequence (K/R/Q)-X_n-(G/S/A/E)-L-G-(F/I/L), wherein X represents any amino acid which is selected from the group comprising the twenty naturally occurring amino acids and n represents at least 2, but not more than 4.

3. The composition of claim 1, wherein the cytoplasmic protein contains the amino acid sequence SLGI.

4. The composition of claim 1, wherein the signal-transducing protein has at its carboxyl terminus the amino acid sequence (S/T)-X-(V/I/L), wherein each - represents a peptide bond, each parenthesis encloses amino acids which are alternatives to one other, each slash within such parentheses separating the alternative amino acids, and the X represents any amino acid which is selected from the group comprising the twenty naturally occurring amino acids.

5. The composition of claim 1, wherein the composition comprises an antibody, an inorganic compound, an organic compound, a peptide, a peptidomimetic

compound, a polypeptide, or a protein.

6. The composition of claim 5, wherein the peptide comprises the sequence (S/T)-X-(V/I/L)-COOH, wherein each - represents a peptide bond, each parenthesis encloses amino acids which are alternatives to one other, each slash within such parentheses separating the alternative amino acids, the X represents any amino acid which is selected from the group comprising the twenty naturally occurring amino acids.

7. The composition of claim 6, wherein the peptide has the amino acid sequence DSENSNFRNEIQSLV.

8. The composition of claim 6, wherein the peptide has the amino acid sequence RNEIQSLV.

9. The composition of claim 6, wherein the peptide has the amino acid sequence NEIQSLV.

10. The composition of claim 6, wherein the peptide has the amino acid sequence EIQSLV.

11. The composition of claim 6, wherein the peptide has the amino acid sequence IQSLV.

12. The composition of claim 6, wherein the peptide has the amino acid sequence QSLV.

13. The composition of claim 6, wherein the peptide has the amino acid sequence SLV.

14. The composition of claim 6, wherein the peptide has the amino acid sequence IPPDSEDGNEEQSLV.

15. The composition of claim 6, wherein the peptide has

the amino acid sequence DSEMYNFRSQLASVV.

16. The composition of claim 6, wherein the peptide has the amino acid sequence IDLASEFLFLSNSFL.

17. The composition of claim 6, wherein the peptide has the amino acid sequence PPTCSQANSGRISTL.

18. The composition of claim 6, wherein the peptide has the amino acid sequence SDSNMNMNELSEV.

19. The composition of claim 6, wherein the peptide has the amino acid sequence QNFRTYIVSFV.

20. The composition of claim 6, wherein the peptide has the amino acid sequence RETIESTV.

21. The composition of claim 6, wherein the peptide has the amino acid sequence RGFISSLV.

22. The composition of claim 6, wherein the peptide has the amino acid sequence TIQSVI.

23. The composition of claim 6, wherein the peptide has the amino acid sequence ESLV.

24. The composition of claim 6, wherein the organic compound has the sequence Ac-SLV-COOH, wherein the Ac represents an acetyl, each - represent a peptide bond.

25. A composition capable of inhibiting specific binding between a signal-transducing protein having at its carboxyl terminus the amino acid sequence (S/T)-X-(V/I/L), wherein each - represents a peptide bond, each parenthesis encloses amino acids which are alternatives to one other, each slash within such

parentheses separating the alternative amino acids, the X represents any amino acid which is selected from the group comprising the twenty naturally occurring amino acids, and a cytoplasmic protein.

26. The composition of claim 25, wherein the composition comprises an antibody, an inorganic compound, an organic compound, a peptide, a peptidomimetic compound, a polypeptide or a protein.

27. A method of identifying a compound capable of inhibiting specific binding between a signal-transducing protein and a cytoplasmic protein containing the amino acid sequence (G/S/A/E)-L-G-(F/I/L), wherein each - represents a peptide bond, each parenthesis encloses amino acids which are alternatives to one other, each slash within such parentheses separating the alternative amino acids, which comprises:

(a) contacting the cytoplasmic protein bound to the signal-transducing protein with a plurality of compounds under conditions permitting binding between a known compound previously shown to be able to displace the signal-transducing protein bound to the cytoplasmic protein and the bound cytoplasmic protein to form a complex; and

(b) detecting the displaced signal-transducing protein or the complex formed in step (a), wherein the displacement indicates that the compound is capable of inhibiting specific binding between the signal-transducing protein and the cytoplasmic protein.

28. The method of claim 27, wherein the inhibition of specific binding between the signal-transducing

protein and the cytoplasmic protein affects the transcription activity of a reporter gene.

29. The method of claim 28, where in step (b) the displaced signal-transducing protein or the complex is detected by comparing the transcription activity of a reporter gene before and after the contacting with the compound in step (a), where a change of the activity indicates that the specific binding between the signal-transducing protein and the cytoplasmic protein is inhibited and the signal-transducing protein is displaced.

30. The method of claim 27, wherein the cytoplasmic protein is bound to a solid support.

31. The method of claim 27, wherein the compound is bound to a solid support.

32. The method of claim 27, wherein the compound comprises an antibody, an inorganic compound, an organic compound, a peptide, a peptidomimetic compound, a polypeptide or a protein.

33. The method of claim 27, wherein the contacting of step (a) is <u>in vitro</u>.

34. The method of claim 27, wherein the contacting of step (a) is <u>in vivo</u>.

35. The method of claim 34, wherein the contacting of step (a) is in a yeast cell.

36. The method of claim 34, wherein the contacting or step (a) is in a mammalian cell.

37. The method of claim 27, wherein the signal-

transducing protein is a cell surface receptor.

38. The method of claim 27, wherein the signal-transducing protein is a signal transducer protein.

39. The method of claim 27, wherein the signal-transducing protein is a tumor suppressor protein.

40. The method of claim 37, wherein the cell surface protein is the Fas receptor.

41. The method of claim 40, wherein the Fas receptor is expressed in cells derived from organs comprising the thymus, liver, kidney, colon, ovary, breast, testis, spleen, stomach, prostate, uterus, skin, head and neck.

42. The method of claim 40, wherein the Fas receptor is expressed in cells comprising T-cells and B-cells.

43. The method of claim 37, wherein the cell-surface receptor is the CD4 receptor.

44. The method of claim 37, wherein the cell-surface receptor is the p75 receptor.

45. The method of claim 37, wherein the cell-surface receptor is the serotonin 2A receptor.

46. The method of claim 37, wherein the cell-surface receptor is the serotonin 2B receptor.

47. The method of claim 38, wherein the signal transducer protein is Protein Kinase-C-α-type.

48. The method of claim 39, wherein the tumor suppressor protein is adenomatosis polyposis coli tumor

suppressor protein.

49. The method of claim 39, wherein the tumor suppressor protein protein is the colorectal mutant cancer protein.

50. The method of claim 27, wherein the cytoplasmic protein contains the amino acid sequence SLGI, wherein each - represents a peptide bond, each parenthesis encloses amino acids which are alternatives to one other, and each slash within such parentheses separating the alternative amino acids.

51. The method of claim 40, wherein the cytoplasmic protein is Fas-associated phosphatase-1.

52. A method of identifying a compound capable of inhibiting specific binding between a signal-transducing protein having at its carboxyl terminus the amino acid sequence (S/T)-X-(V/I/L), wherein each - represents a peptide bond, each parenthesis encloses amino acids which are alternatives to one other, each slash within such parentheses separating the alternative amino acids, the X represents any amino acid which is selected from the group comprising the twenty naturally occurring amino acids, and a cytoplasmic protein, which comprises:

(a) contacting the signal-transducing protein bound to the cytoplasmic protein with a plurality of compounds under conditions permitting binding between a known compound previously shown to be able to displace the cytoplasmic protein bound to the signal-transducing protein and the bound signal-transducing protein to form a complex; and

(b) detecting the displaced cytoplasmic protein or the complex of step (a) wherein the displacement indicates that the compound is capable of inhibiting specific binding between the signal-transducing protein and the cytoplasmic protein.

53. The method of claim 52, wherein the inhibition of specific binding between the signal-transducing protein and the cytoplasmic protein affects the transcription activity of a reporter gene.

54. The method of claim 53, where in step (b) the displaced cytoplasmic protein or the complex is detected by comparing the transcription activity of a reporter gene before and after the contacting with the compound in step (a), where a change of the activity indicates that the specific binding between the signal-transducing protein and the cytoplasmic protein is inhibited and the cytoplasmic protein is displaced.

55. The method of claim 52, wherein the cytoplasmic protein is bound to a solid support.

56. The method of claim 52, wherein the compound is bound to a solid support.

57. The method of claim 52, wherein the compound comprises an antibody, an inorganic compound, an organic compound, a peptide, a peptidomimetic compound, a polypeptide or a protein.

58. The method of claim 52, wherein the contacting of step (a) is <u>in vitro</u>.

59. The method of claim 52, wherein the contacting of

step (a) is in vivo.

60. The method of claim 59, wherein the contacting of step (a) is in a yeast cell.

61. The method of claim 59, wherein the contacting or step (a) is in a mammalian cell.

62. The method of claim 52, wherein the signal-transducing protein is a cell surface receptor.

63. The method of claim 52, wherein the signal-transducing protein is a signal transducer protein.

64. The method of claim 52, wherein the signal-transducing protein is a tumor suppressor protein.

65. The method of claim 62, wherein the cell surface protein is the Fas receptor.

66. The method of claim 65, wherein the Fas receptor is expressed in cells derived from organs comprising the thymus, liver, kidney, colon, ovary, breast, testis, spleen, stomach, prostate, uterus, skin, head and neck.

67. The method of claim 65, wherein the Fas receptor is expressed in cells comprising T-cells and B-cells.

68. The method of claim 62, wherein the cell-surface receptor is the CD4 receptor.

69. The method of claim 62, wherein the cell-surface receptor is the p75 receptor.

70. The method of claim 62, wherein the cell-surface receptor is the serotonin 2A receptor.

71. The method of claim 62, wherein the cell-surface receptor is the serotonin 2B receptor.

72. The method of claim 63, wherein the signal transducer protein is Protein Kinase-C-α-type.

73. The method of claim 64, wherein the tumor suppressor protein is adenomatosis polyposis coli tumor suppressor protein.

74. The method of claim 64, wherein the tumor suppressor protein is the colorectal mutant cancer protein.

75. The method of claim 52, wherein the cytoplasmic protein contains the amino acid sequence SLGI, wherein each - represents a peptide bond, each parenthesis encloses amino acids which are alternatives to one other, and each slash within such parentheses separating the alternative amino acids.

76. The method of claim 52, wherein the cytoplasmic protein is Fas-associated phosphatase-1.

77. A method inhibiting the proliferation of cancer cells comprising the composition of claim 1.

78. The method of claim 77, wherein the cancer cells are derived from organs comprising the thymus, liver, kidney, colon, ovary, breast, testis, spleen, stomach, prostate, uterus, skin, head and neck.

79. The method of claim 77, wherein the cancer cells are derived from cells comprising T-cells and B-cells.

80. A method of inhibiting the proliferation of cancer

cells comprising the composition of claim 25.

81. The method of claim 80, wherein the cancer cells are derived from organs comprising the thymus, liver, kidney, colon, ovary, breast, testis, spleen, stomach, prostate, uterus, skin, head and neck.

82. The method of claim 80, wherein the cancer cells are derived from cells comprising T-cells and B-cells.

83. A method of inhibiting the proliferation of cancer cells comprising the compound identified by the method of claim 27.

84. The method of claim 83, wherein the cancer cells are derived from organs comprising the thymus, liver, kidney, colon, ovary, breast, testis, spleen, stomach, prostate, uterus, skin, head and neck.

85. The method of claim 83, wherein the cancer cells are derived from cells comprising T-cells and B-cells.

86. A method of inhibiting the proliferation of cancer cells comprising the compound identified by the method of claim 52.

87. The method of claim 86, wherein the cancer cells are derived from organs comprising the thymus, liver, kidney, colon, ovary, breast, testis, spleen, stomach, prostate, uterus, skin, head and neck.

88. The method of claim 86, wherein the cancer cells are derived from cells comprising T-cells and B-cells.

89. A method of treating cancer in a subject which comprises introducing to the subject's cancerous cells an amount of the composition of claim 1

effective to result in apoptosis of the cells.

90. The method of claim 89, wherein the cancer cells are derived from organs comprising the thymus, liver, kidney, colon, ovary, breast, testis, spleen, stomach, prostate, uterus, skin, head and neck.

91. The method of claim 89, wherein the cancer cells are derived from cells comprising T-cells and B-cells.

92. A method of treating cancer in a subject which comprises introducing to the subject's cancerous cells an amount of the composition of claim 25 effective to result in apoptosis of the cells.

93. The method of claim 92, wherein the cancer cells are derived from organs comprising the thymus, liver, kidney, colon, ovary, breast, testis, spleen, stomach, prostate, uterus, skin, head and neck.

94. The method of claim 92, wherein the cancer cells are derived from cells comprising T-cells and B-cells.

95. A method of treating cancer in a subject which comprises introducing to the subject's cancerous cells an amount of the compound identified by the method of claim 27 effective to allow apoptosis of the cells.

96. The method of claim 95, wherein the cancer cells are derived from organs comprising the thymus, liver, kidney, colon, ovary, breast, testis, spleen, stomach, prostate, uterus, skin, head and neck.

97. The method of claim 95, wherein the cancer cells are derived from cells comprising T-cells and B-cells.

98. A method of treating cancer in a subject which comprises introducing to the subject's cancerous cells an amount of the compound identified by the method of claim 52 effective to result in apoptosis of the cells.

99. The method of claim 98, wherein the cancer cells are derived from organs comprising the thymus, liver, kidney, colon, ovary, breast, testis, spleen, stomach, prostate, uterus, skin, head and neck.

100. The method of claim 98, wherein the cancer cells are derived from cells comprising T-cells and B-cells.

101. A method of inhibiting the proliferation of virally infected cells comprising the composition of claim 1.

102. A method of inhibiting the proliferation of virally infected cells comprising the composition of claim 25.

103. A method of inhibiting the proliferation of virally infected cells comprising the compound identified by the method of claim 27.

104. A method of inhibiting the proliferation of virally infected cells comprising the compound identified by the method of claim 52.

105. The method of claim 101, wherein the virally infected cells comprise Hepatitis B virus, Epstein-Barr virus, influenza virus, Papilloma virus. Adeno virus, Human T-cell lymphtropic virus, type 1 or HIV.

106. The method of claim 102, wherein the virally

infected cells comprise Hepatitis B virus, Epstein-Barr virus, influenza virus, Papilloma virus. Adeno virus, Human T-cell lymphtropic virus, type 1 or HIV.

107. The method of claim 103, wherein the virally infected cells comprise Hepatitis B virus, Epstein-Barr virus, influenza virus, Papilloma virus. Adeno virus, Human T-cell lymphtropic virus, type 1 or HIV.

108. The method of claim 104, wherein the virally infected cells comprise Hepatitis B virus, Epstein-Barr virus, influenza virus, Papilloma virus. Adeno virus, Human T-cell lymphtropic virus, type 1 or HIV.

109. A method of treating a virally-infected subject which comprises introducing to the subject's virally- infected cells the composition of claim 1 effective to result in apoptosis of the cells.

110. A method of treating a virally-infected subject which comprises introducing to the subject's virally infected cells the composition of claim 25 effective to result in apoptosis of the cells.

111. A method of treating a virally-infected subject which comprises introducing to the subject's virally-infected cells an amount of the compound identified by the method of claim 27 effective to result in apoptosis of the cells.

112. A method of treating a virally-infected subject which comprises introducing to the subject's virally- infected cells an amount of the compound identified by the method of claim 52 effective to

result in apoptosis of the cells.

113. The method of claim 109, wherein the virally infected cells comprise the Hepatitis B virus, Epstein-Barr virus, influenza virus, Papilloma virus. Adeno virus, Human T-cell lymphtropic virus, type 1 or HIV.

114. The method of claim 110, wherein the virally infected cells comprise the Hepatitis B virus, Epstein-Barr virus, influenza virus, Papilloma virus. Adeno virus, Human T-cell lymphtropic virus, type 1 or HIV.

115. The method of claim 111, wherein the virally infected cells comprise the Hepatitis B virus, Epstein-Barr virus, influenza virus, Papilloma virus. Adeno virus, Human T-cell lymphtropic virus, type 1 or HIV.

116. The method of claim 112, wherein the virally infected cells comprise the Hepatitis B virus, Epstein-Barr virus, influenza virus, Papilloma virus. Adeno virus, Human T-cell lymphtropic virus, type 1 or HIV.

117. A pharmaceutical composition comprising the composition of claim 1 in an effective amount and a pharmaceutically acceptable carrier.

118. A pharmaceutical composition comprising the composition of claim 25 in an effective amount and a pharmaceutically acceptable carrier.

119. A pharmaceutical composition comprising the compound identified by the method of claim 27 in an effective amount and a pharmaceutically acceptable carrier.

120. A pharmaceutical composition comprising the compound identified by the method of claim 52 in an effective amount and a pharmaceutically acceptable carrier.

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